Amendments to the Specification

Please replace paragraphs [0144] and [0145] with the following amended paragraphs.

[0144] Total RNA was isolated from young pepper leaves using Trizol reagant (Invitrogen, Carlsbad, CA) following the manufacturer's instructions. RNA blots were done according to standard methods (Sambrook et al., "Molecular Cloning : A Laboratory Manual," Third Edition, Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (2001), which is hereby incorporated by reference in its entirety). First strand cDNA was synthesized in 25 µl containing 2µg total RNA and 500 ng oligo dT using M-MLV reverse transcriptase (Promega, Madison, WI) according to the manufacturer's instructions. For RT-PCR, 2 µl of cDNA was added to a reaction volume of 25 µl containing 10 mM KCl, 10 mM $(NH_4)_2SO_4$, 20 mM Tris-HCl, 2 mM $MgSO_4$, 0.1% Triton X-100, 0.2 mM each dNTP, 0.4 [[uM]] µM each forward and reverse primer, and 1 unit *Taq* polymerase (New England Biolabs, Beverly, MA). PCR cycling conditions were 95°C 3 m, (95°C 30 s, 55°C 30 s, 72°C 5 m) x 1, (95°C 30 s, 55°C 30 s, 72°C 90 s) x 29, 72°C 10 min. Full-length eIF4E-687 ORF primers (forward 5′-ATGGCAACAGCTGAAATGG-3′ (SEQ ID NO:9); reverse 5′-TATACGGTGTAACGATTCTTGGCA-3′ (SEQ ID NO:10) were based on tomato eIF4E sequence (Genbank accession AF259801). Full-length eIF(iso)4E ORF primers (forward 5′-AACAATGGCCACCGAAGC-3′ (SEQ ID NO:15); reverse 5′-ATTTCACAGTATATCGGCTCT-3′ (SEQ ID NO:16)) were based on published tomato sequence (TIGR accession TC103222) (~~www.tigr.org~~). Full-length eIF4E-537 ORF primers (forward 5′-TTAGGCAAACCAATCACAATG-3′ (SEQ ID NO:19); reverse 5′-CCTGTTGTAACGATAGAACTA-3′ (SEQ ID NO:20)) were based on published tomato sequence (TIGR accession TC96888). PCR products were run on 1.5% agarose. Gel slices were purified using the Qiaquick gel purification kit (Qiagen, Valencia, CA) and cloned using the pGEM-T Easy kit (Promega, Madison, WI).

[0145] At least two positive clones were sequenced from both ends for each PCR product and analyzed using Seqman software (DNASTAR Inc., Madison, WI.). Amino acid sequence

alignments were produced using the Clustal algorithm within Megalign software (DNASTAR). For protein homology models, pepper sequence was submitted to the SwissProt database via the application DeepView ~~(www.expasy.ch/spdbv/text/server.htm)~~. The model was generated using the murine crystal structure for eIF4E (sequence 1EJ1.B).